

2009-11-22 0425-1257PUS1_ST25 (2)
SEQUENCE LISTING

<110> MACHIDA, Kazuhiro et al.
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<140> US 10/577,655
<141> 2006-05-01
<150> JP 2003-396828
<151> 2003-11-27
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Met Thr Glu Leu Thr Asp Ile Thr Gly Pro Gly Thr Pro Ala Glu Pro							
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Val Ala Phe Pro Gln Asp Arg Thr Cys Pro Tyr His Pro Pro Thr Gly							
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Tyr Gly Pro Leu Arg Asp Gly Arg Ser Leu Ser Arg Val Thr Leu Phe							
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Pro Val Pro Thr Ala Arg Phe Ala Ala Val Arg Asp Arg Arg Val Ala							
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100 105 110							
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Gln Arg Thr Val Asp Gly Leu Leu Asp Ala Met Ile Glu Lys Gly Pro							
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Ile Cys Gly Leu Leu Gly Val Pro Tyr Ala Asp His Glu Phe Phe Glu							
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Lys	Glu	Arg	Gln	Ala	Glu	Pro	Gly	Asp	Gly	Val	Leu	Asp	Asp	Leu	Val		
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His	Gln	Arg	Leu	Arg	Thr	Gly	Glu	Leu	Asp	Arg	Arg	Asp	Val	Val	Val	Ala	
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Phe	Ser	Thr	Ser	Leu	Ile	Asn	Arg	Asp	Glu	Ser	Val	Phe	Asp	Asp	Pro		
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Gly	Met	Leu	Glu	Leu	Pro	Val	Thr	Trp									
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gac	atc	gac	aag	gac	cgc	tgc	atc	ggc	gcc	gac	tgc	cg	ctg	gcc			2620
Asp	Ile	Asp	Lys	Asp	Arg	Cys	Ile	Gly	Ala	Gly	Gly	Cys	Ala	Leu	Ala		
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gcc	ccg	ggc	gtg	ttc	acc	cag	gac	gac	gac	ggc	tac	acg	acc	ctg	ctc		2668
Ala	Pro	Gly	Val	Phe	Thr	Gln	Asp	Asp	Asp	Gly	Tyr	Ser	Thr	Leu	Leu		
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Ile Pro Ser Phe Thr Leu Lys Arg Ala Ala Gly Leu Arg Pro Thr Ile
115 120 125

Gln Arg Thr Val Asp Gly Leu Leu Asp Ala Met Ile Glu Lys Gly Pro
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Ile Ser Leu Gly Thr Tyr Thr Leu Leu Arg His Pro Gly Arg Leu Ala
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Glu Leu Arg Ala Asp Pro Ala Leu Leu Pro Ala Ala Val Glu Glu Leu
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Met Arg Met Leu Ser Ile Ala Asp Gly Leu Leu Arg Leu Ala Leu Glu
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325 330 335

Asp Thr Leu Asp Phe His Arg Ser Thr Arg His His Val Ala Phe Gly
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Phe Gly Ile His Gln Cys Leu Gly Gln Asn Leu Ala Arg Ala Glu Leu
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Glu Ile Ala Leu Gly Thr Leu Leu Glu Arg Leu Pro Gly Leu Arg Leu
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Pro Pro Ala Ala Tyr Gln Pro Leu Arg Gly Ala Gly Pro Leu Ser His 20 25 30

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Val Thr Phe Tyr Asp Gly Arg Lys Val Trp Ala Val Thr Gly His Pro 35 40 45

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Glu Ala Arg Ala Leu Leu Thr Asp Gln Arg Leu Ser Ala Asp Arg Gln 50 55 60

aac ccg gcc ttc ccg gtc ccc ttc gaa cgc ttc gcg gcc atc cgc cgg 659
Asn Pro Ala Phe Pro Val Pro Phe Glu Arg Phe Ala Ala Ile Arg Arg 65 70 75 80

gtc cgg acg ccg ctg atc ggg gtc gac gac ccg gag cac aac acc cag 707
Val Arg Thr Pro Leu Ile Gly Val Asp Asp Pro Glu His Asn Thr Gln 85 90 95

cgc cgg atg ctg atc ccc agc ttc agc ctc aag cgg acc gcc gca ctg 755
Arg Arg Met Leu Ile Pro Ser Phe Ser Leu Lys Arg Thr Ala Ala Leu 100 105 110

ccg ccg gag atc cag cgg atc gtc gac ggg ctg ctc gac cgg atg ctg 803
Arg Pro Glu Ile Gln Arg Ile Val Asp Gly Leu Leu Asp Arg Met Leu 115 120 125

gat cag ggc ccg ccc acc gag ctg gtc tcc gcg ttc gcc ctg ccg gtc 851
Asp Gln Gly Pro Pro Thr Glu Leu Val Ser Ala Phe Ala Leu Pro Val 130 135 140

ccg tcg atg gtg atc tgc gca ctg ctc gga gtc tca tac gcc gac cat 899
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gag	ctg	ctg	cga	ttc	ctg	tcc	atc	gcg	gac	ggc	ctg	ctg	cgg	gtg	gcg	1283
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Thr	Glu	Asp	Ile	Glu	Ile	Gly	Gly	Gln	Val	Ile	Arg	Ala	Asp	Asp	Ala	
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Val	Leu	Phe	Pro	Ala	Ser	Leu	Ile	Asn	Arg	Asp	Glu	Ala	Ala	Tyr	Pro	
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Ala	Pro	Asp	Glu	Leu	Asp	Leu	Gly	Arg	Ser	Ala	Arg	His	His	Val	Ala	
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Leu	Gln	Gly	Met	Ile	Glu	Leu	Pro	Leu	Ala	Trp						
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gac ccg ctg gtg cg ^g gaa gcc gcc cgc gcc tgc ccc gtg cag gcc att Asp Pro Leu Val Arg Glu Ala Ala Arg Ala Cys Pro Val Gln Ala Ile 440 445 450	1819
g ^c g gtc acc gac gat tagcagcacc cccgggacg acccggcaga cgcgcgcc Ala Val Thr Asp Asp 455	1874
ccccggctgac acccggcgcc cgaggcg ^c c ^c cgagccgtc cgccccc ^t cca cttgtcccta cg ^g catccac cccatccgct accgcaaacac cccttgggtg acgggcagtt tcgaggaccc cggtgtgccc ggggcgtact ggtgaccgtc accggcttca cgccgcgatt gcccacata ^g gcgtcg ^t gc tcgcggcgat cacgaagcgc ggtcggtgcc cccgctcgta acggtgac ^c g atgccccggca gttccacgg ^t gaaccggccgg g ^c ccacatcg ^g gcacccgggc cggggccacc aacaggtgca ccagcgtctt cctgccc ^t tc ggcgcgacat cgttagagctt ggcgaacagc accagcttgtt ccgcccgc ^t atc cgcggaccgc tgccccc ^t cc cggcctgcgg cgaggcaacc ttcagcgtca ccctcg ^c g ^c gc gcccaccacg tcgac	1934
<210> 5 <211> 395 <212> PRT <213> Streptomyces sp.	1994
<400> 5	2054
Val Thr Glu Ala Ile Pro Tyr Phe Gln Asn Arg Thr Cys Pro Tyr His 1 5 10 15	2114
Pro Pro Ala Ala Tyr Gln Pro Leu Arg Gly Ala Gly Pro Leu Ser His 20 25 30	2174
Val Thr Phe Tyr Asp Gly Arg Lys Val Trp Ala Val Thr Gly His Pro 35 40 45	2234
Glu Ala Arg Ala Leu Leu Thr Asp Gln Arg Leu Ser Ala Asp Arg Gln 50 55 60	2294
Asn Pro Ala Phe Pro Val Pro Phe Glu Arg Phe Ala Ala Ile Arg Arg 65 70 75 80	2329

Val Arg Thr Pro Leu Ile Gly Val Asp Asp Pro Glu His Asn Thr Gln
85 90 95

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Arg Arg Met Leu Ile Pro Ser Phe Ser Leu Lys Arg Thr Ala Ala Leu
100 105 110

Arg Pro Glu Ile Gln Arg Ile Val Asp Gly Leu Leu Asp Arg Met Leu
115 120 125

Asp Gln Gly Pro Pro Thr Glu Leu Val Ser Ala Phe Ala Leu Pro Val
130 135 140

Pro Ser Met Val Ile Cys Ala Leu Leu Gly Val Ser Tyr Ala Asp His
145 150 155 160

Glu Phe Phe Glu Glu Ser Arg Arg Ile Leu Arg Gly Arg Ser Ala
165 170 175

Glu Glu Ala Glu Asp Ala Arg Leu Lys Leu Glu Glu Tyr Phe Thr Gly
180 185 190

Leu Ile Ala Ala Lys Glu Lys Asn Pro Gly Asp Gly Leu Leu Asp Glu
195 200 205

Leu Ile Glu Asp Arg Leu Arg Thr Gly Ala Leu Thr Arg Asp Glu Leu
210 215 220

Val Arg Leu Ala Met Ile Leu Leu Val Ala Gly His Glu Thr Thr Ala
225 230 235 240

Asn Met Ile Ser Leu Gly Thr Phe Thr Leu Leu Asp His Pro Glu Gln
245 250 255

Leu Ala Gln Leu Lys Ala Asp Glu Gly Leu Met Pro Ala Ala Ile Glu
260 265 270

Glu Leu Leu Arg Phe Leu Ser Ile Ala Asp Gly Leu Leu Arg Val Ala
275 280 285

Thr Glu Asp Ile Glu Ile Gly Gly Gln Val Ile Arg Ala Asp Asp Ala
290 295 300

Val Leu Phe Pro Ala Ser Leu Ile Asn Arg Asp Glu Ala Ala Tyr Pro
305 310 315 320

Ala Pro Asp Glu Leu Asp Leu Gly Arg Ser Ala Arg His His Val Ala
325 330 335

Ser Gly Phe Gly Ile His Gln Cys Leu Gly Gln Asn Leu Ala Arg Ala
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340

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345
350

Glu Met Glu Ile Ala Leu Arg Ser Leu Phe Thr Arg Ile Pro Gln Leu
355 360 365

Arg Leu Ala Val Pro Ala Ala Glu Ile Pro Phe Lys Asp Gly Asp Thr
370 375 380

Leu Gln Gly Met Ile Glu Leu Pro Leu Ala Trp
385 390 395

<210> 6
<211> 64
<212> PRT
<213> Streptomyces sp.

<400> 6

Met Arg Ile Ala Ile Asp Thr Asp Arg Cys Ile Gly Ala Gly Gln Cys
1 5 10 15

Ala Leu Thr Ala Pro Gly Gly Phe Thr Gln Asp Asp Asp Gly Phe Ser
20 25 30

Ala Leu Leu Pro Gly Arg Glu Asp Gly Ala Gly Asp Pro Leu Val Arg
35 40 45

Glu Ala Ala Arg Ala Cys Pro Val Gln Ala Ile Ala Val Thr Asp Asp
50 55 60

<210> 7
<211> 1860
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Sequence: nucleotide sequence with coding
region derived from an unknown source

<220>
<221> CDS
<222> (172)..(1383)

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<222> (1399)..(1593)

<400> 7
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ccagccagat cccgcaggta gccgatctgg ccgaacttga tgtcgtgcac tggatgcctc 120
gggcattcaa tgaagatcgg cacgacgcat ccttcgtctg cgaggtctcc c atg aca 177
Met Thr

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1

gac acg aca gac ctg acc gag ctg tca gat ccc gtc tcc ttc ccc cag Asp Thr Thr Asp Leu Thr Glu Leu Ser Asp Pro Val Ser Phe Pro Gln 5 10 15	225
gac cgg agc tgc ccc tac cac ccg ccc acc ggg tac gac ccg ctg cgc Asp Arg Ser Cys Pro Tyr His Pro Pro Thr Gly Tyr Asp Pro Leu Arg 20 25 30	273
acc gaa cg ^g ccg ccc gcc cgc atc cg ^g ctc tac gac ggc cgc ccc gcc Thr Glu Arg Pro Pro Ala Arg Ile Arg Leu Tyr Asp Gly Arg Pro Ala 35 40 45 50	321
tgg ctc gtc acc ggc cac gcc gtc gcc cgt gac ctg ctg gtc gac ccc Trp Leu Val Thr Gly His Ala Val Ala Arg Asp Leu Leu Val Asp Pro 55 60 65	369
cgc ctg tcc acg gac cgc acc cgc tcg ggc ttc ccg gcc aca act ccc Arg Leu Ser Thr Asp Arg Thr Arg Ser Gly Phe Pro Ala Thr Thr Pro 70 75 80	417
cgc ttc gcc gc ^g gtc cgc gac cgc aag ccg gc ^g ctc ctc ggc gtc gac Arg Phe Ala Ala Val Arg Asp Arg Lys Pro Ala Leu Leu Gly Val Asp 85 90 95	465
gac ccc aag cac cgc acc cag cg ^g tgg atg atg atc ccg agc ttc acc Asp Pro Lys His Arg Thr Gln Arg Trp Met Met Ile Pro Ser Phe Thr 100 105 110	513
ctc agg cgc gcc acc gag ctc agg ccg cgc atc cag gag atc gtc gac Leu Arg Arg Ala Thr Glu Leu Arg Pro Arg Ile Gln Glu Ile Val Asp 115 120 125 130	561
gaa ctg ctg gac gtg atg atc gcc cag gga ccc ccg gcc gac ctg gtg Glu Leu Leu Asp Val Met Ile Ala Gln Gly Pro Pro Ala Asp Leu Val 135 140 145	609
cgt tcc ttc gc ^g ctg ccg gtg ccg tcc atg gtg atc tgc gcc ctg ctc Arg Ser Phe Ala Leu Pro Val Pro Ser Met Val Ile Cys Ala Leu Leu 150 155 160	657
ggc gtg ccc tac gcc gac cac gag ttc ttc gag gac cag tcc agg cgg Gly Val Pro Tyr Ala Asp His Glu Phe Phe Glu Asp Gln Ser Arg Arg 165 170 175	705
ctg ctg cgc gga ccg gc ^g gcc gag gac acg cag gac gcc ccg gac cgg Leu Leu Arg Gly Pro Ala Ala Glu Asp Thr Gln Asp Ala Arg Asp Arg 180 185 190	753
ctc gcc gc ^g tac ctg gag gac ctg atc gac gag aag cgg cgc cgg ccc Leu Ala Ala Tyr Leu Glu Asp Leu Ile Asp Glu Lys Arg Arg Arg Pro 195 200 205 210	801
ggt gac ggc ctg ctg gac gaa ctc gtc cag cag cgt ctg aac gaa ggc Gly Asp Gly Leu Leu Asp Glu Leu Val Gln Gln Arg Leu Asn Glu Gly 215 220 225	849
gag ctc gac cgg gag gaa ctg acc gc ^g ctg gc ^g atg atc ctg ctg gtc Glu Leu Asp Arg Glu Glu Leu Thr Ala Leu Ala Met Ile Leu Leu Val 230 235 240	897
g ^c gc ggc cac gag acc acc gcc aac atg atc tcc ctg ggc acc tac acg	945

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aagccctccg gggcgccgccc cgcgaaagac accggggacgg cgcccgaa accccttcct 1803
ctacgtcgtc gtctgcgccc ccggcatcgc cgaaggcgta agcaagctga tcaccgc 1860

<210> 8
<211> 404
<212> PRT
<213> Unknown

<220>
<223> Derived from an unknown source

<400> 8

Met Thr Asp Thr Thr Asp Leu Thr Glu Leu Ser Asp Pro Val Ser Phe
1 5 10 15

Pro Gln Asp Arg Ser Cys Pro Tyr His Pro Pro Thr Gly Tyr Asp Pro
20 25 30

Leu Arg Thr Glu Arg Pro Pro Ala Arg Ile Arg Leu Tyr Asp Gly Arg
35 40 45

Pro Ala Trp Leu Val Thr Gly His Ala Val Ala Arg Asp Leu Leu Val
50 55 60

Asp Pro Arg Leu Ser Thr Asp Arg Thr Arg Ser Gly Phe Pro Ala Thr
65 70 75 80

Thr Pro Arg Phe Ala Ala Val Arg Asp Arg Lys Pro Ala Leu Leu Gly
85 90 95

Val Asp Asp Pro Lys His Arg Thr Gln Arg Trp Met Met Ile Pro Ser
100 105 110

Phe Thr Leu Arg Arg Ala Thr Glu Leu Arg Pro Arg Ile Gln Glu Ile
115 120 125

Val Asp Glu Leu Leu Asp Val Met Ile Ala Gln Gly Pro Pro Ala Asp
130 135 140

Leu Val Arg Ser Phe Ala Leu Pro Val Pro Ser Met Val Ile Cys Ala
145 150 155 160

Leu Leu Gly Val Pro Tyr Ala Asp His Glu Phe Phe Glu Asp Gln Ser
165 170 175

Arg Arg Leu Leu Arg Gly Pro Ala Ala Glu Asp Thr Gln Asp Ala Arg
180 185 190

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Asp Arg Leu Ala Ala Tyr Leu Glu Asp Leu Ile Asp Glu Lys Arg Arg
195 200 205

Arg Pro Gly Asp Gly Leu Leu Asp Glu Leu Val Gln Gln Arg Leu Asn
210 215 220

Glu Gly Glu Leu Asp Arg Glu Glu Leu Thr Ala Leu Ala Met Ile Leu
225 230 235 240

Leu Val Ala Gly His Glu Thr Thr Ala Asn Met Ile Ser Leu Gly Thr
245 250 255

Tyr Thr Leu Leu Leu His Pro Glu Arg Leu Thr Glu Leu Arg Ala Asp
260 265 270

Pro Ala Leu Leu Pro Ala Ala Val Glu Glu Leu Met Arg Met Leu Ser
275 280 285

Ile Ala Asp Gly Leu Leu Arg Gln Ala Thr Glu Asp Ile Glu Ile Ala
290 295 300

Gly Thr Thr Ile Arg Ala Gly Asp Gly Val Val Phe Ser Thr Ser Val
305 310 315 320

Ile Asn Arg Asp Glu Asp Val Tyr Pro Ala Pro Asp Thr Leu Asp Phe
325 330 335

His Arg Ser Thr Arg His His Val Ala Phe Gly Phe Gly Ile His Gln
340 345 350

Cys Leu Gly Gln Asn Leu Ala Arg Thr Glu Leu Glu Ile Ala Leu Arg
355 360 365

Thr Leu Leu Glu Arg Leu Pro Thr Leu Arg Leu Ala Ala Pro Pro Glu
370 375 380

Glu Ile Pro Phe Lys Pro Gly Asp Thr Ile Gln Gly Met Leu Glu Leu
385 390 395 400

Pro Val Ser Trp

<210> 9
<211> 65
<212> PRT
<213> Unknown

<220>
<223> Derived from an unknown source

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<400> 9

Met His Ile Glu Ile Asp Lys Asp Arg Cys Ile Gly Ala Gly Gln Cys
1 5 10 15

Ala Leu Thr Ala Pro Gly Val Phe Thr Gln Asp Asp Asp Gly Phe Ser
20 25 30

Asp Leu Leu Pro Gly Arg Glu Asp Gly Ala Gly Asp Pro Met Val Arg
35 40 45

Glu Ala Ala Arg Ala Cys Pro Val Ser Ala Ile Thr Leu Ser Glu Asp
50 55 60

Gly
65

<210> 10

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : 5Dm-3F Primer

<400> 10

ttcgcscctsc csgtcccstc satggtsat

29

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : 5Dm-3R Primer

<400> 11

gttgatctttt gasgtsgaga a

21

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : 6PIN-2F Primer

<400> 12

gctgcgcctg gccctggagg acatcgagat

30

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence : 6PIN-2R Primer

<400> 13
ctgttcctcg aagaactcgt ggtcggcgta 30

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : DM-NdeF Primer

<400> 14
gccccccatcat gacggaactg acggacatca 30

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : DM-SpeR Primer

<400> 15
gggccactag tcagccggcc ggttcggtca 30

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : DM-BglF Primer

<400> 16
cgcataatc ttcacccgag cgggtgatca 30

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : DM-BglR Primer

<400> 17
tcccggatc ttgaagggtcc gcgtcaccgt 30

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 5D-1R Primer

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<400> 18
agggtccccag cgagatcatg tt 22

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 7PIN-2F Primer

<400> 19
ccatgatcct gctggtggcc ggccatgaga 30

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 07-NdeF Primer

<400> 20
gccccatatg accgaaggca tcccctactt 30

<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 07-SpeR Primer

<400> 21
gccactagtg ctaatcgctcg gtgaccgcaa 30

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 5Dm-2R Primer

<400> 22
ctggatsgtg tcscsggyt t 21

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : 5PIN-2F Primer

<400> 23
cggaatccac cagtgcctcg gccagaacct 30

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<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : tpm-NdeF Primer

<400> 24
ggcccatat gacagacacg acagacctga 30

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : tpm-SpeR Primer

<400> 25
gcgcgactag tccccctacc cgtcctcgga 30